

# Integration of Queueing Network into Susceptible Exposed Likely Infected Confirmed Dead Removed Model for Ebola Virus Disease Analysis

Ikeme John Dike<sup>1\*</sup>, Chinyere Ogochukwu Dike<sup>2</sup>

<sup>1</sup>Department of Statistics & Operations Research, Modibbo Adama University of Technology, P.M.B 2076, Yola, Adamawa State, Nigeria

<sup>2</sup>Federal College of Education P.M.B 2042, Yola, Adamawa State, Nigeria

\*Corresponding author: [dikeij@gmail.com](mailto:dikeij@gmail.com)

**Abstract** Ebola Virus Disease (EVD) is a complicated and unparalleled epidemic disease. In recent times, the disease has been ravaging human lives and economy in West African nations. The most affected countries are Guinea, Liberia and Sierra Leone. Contagious disease like Ebola transmits through networks, made by bodily interactions among persons. As a result of the transmission mode and deadly nature of the disease, this paper proposes an EVD transmission and control model which incorporates queueing network that considers all the transmission phases in order to understand the real nature of the disease and predict its behaviour. The result for network indicates that the population was vulnerable to large scale epidemics before intervention in the three countries. In network model, critical transmissibility or epidemic threshold  $T_C$  is the least transmissibility necessary for an outbreak to turn into a large scale epidemic. The  $T_C$  for the three countries was 0.0644. Before intervention, the transmissibility for Guinea was 0.1365, Liberia, 0.2093 and Sierra Leone, 0.1325. After intervention, the transmissibility for Guinea became 0.0595, Liberia, 0.0440 and Sierra Leone, 0.0571. The before and after transmissibility results in comparison with the  $T_C$  indicate that intervention was effective in containing the EVD epidemic. The vulnerability decreased drastically after intervention.

**Keywords:** Ebola virus disease, epidemic, queueing network, transmission, control

**Cite This Article:** Ikeme John Dike, and Chinyere Ogochukwu Dike, "Integration of Queueing Network into Susceptible Exposed Likely Infected Confirmed Dead Removed Model for Ebola Virus Disease Analysis." *American Journal of Applied Mathematics and Statistics*, vol. 6, no. 2 (2018): 54-60. doi: 10.12691/ajams-6-2-3.

## 1. Introduction

Ebola Virus Disease has unique transmission phases, namely: Susceptible, Exposed, Likely Infected, Confirmed Infected, Dead, Removed-SEI<sub>L</sub>I<sub>C</sub>DR [6]. Contagious disease like Ebola transmits through networks, made by bodily interactions among persons. Nevertheless, EVD is a contagious epidemic case with high transmission rate once an outbreak occurs. Hence, open queueing network is applicable in EVD epidemic, since open queueing networks are systems in which infected person are able to enter and depart the system [21]. This can be justified from the developed SEI<sub>L</sub>I<sub>C</sub>DR model which is an open queueing network. Infected individual move from Susceptible to Exposed, to Likely Infected, to Confirm Infected and finally either Die or Recover. The transmission of EVD is a system with a random, unsequential and multiple disorder pattern. This paper applies the principles of multiple channel open Jackson queueing networks to describe the EVD transmission dynamics. The network involves the multiple contact stations. An urban contact network offers a high degree of realism, which involves stations like

households, shopping centres, religious centres, schools, workplaces, hospitals and so on in a given community.

Queueing theory is the mathematical study of waiting lines, or queues [24]. As a result of the transmission mode and deadly nature of the disease, this paper incorporates network into the SEI<sub>L</sub>I<sub>C</sub>DR model that considers all the transmission phases in order to understand the real nature of the disease and predict its behaviour.

## 2. Network Model

### 2.1. SEI<sub>L</sub>I<sub>C</sub>DR Queueing Networks

The principle of queueing networks assumes that the treatment of an individual in an epidemic transmission/control system is not complete until the individual has passed through all the available stages or states [21]. For instance, in SEI<sub>L</sub>I<sub>C</sub>DR model an individual has to pass through the  $S \rightarrow E \rightarrow I_L \rightarrow I_C \rightarrow D/R$  stages. The transmission of EVD is a system with a random, unsequential, and multiple disorder patterns. Therefore, multiple channel open Jackson queueing networks was applied in this paper.

## 2.2. Multiple Channel Open Jackson Queueing Networks

Interconnected collection of stations is defined as queueing networks, that is, inventions with queues, in which there is movement of jobs from one station to the subsequent station demanding service. Over the last five decades queueing networks have been known as models of manufacturing computer and communication systems. Jackson [12]; Gordon and Newell [7] indicate that open and closed networks with one job class, exponential service time distributions and First Come First Served (FCFS) scheduling in all stations have product form solution. Multiple job classes in open, mixed and closed networks is an extension by Kelly [13]. Baskett et al [1] give product form solutions for service requirement distributions that have rational Laplace transforms, denoted by stages. Multiple job classes can be suitable, and the service necessity distributions can rely on the class. Multitask performance is treated by single channel, serial processing models as an issue of task selection and scheduling. The multiple channel, parallel processing models in contrast, treat multitask performance as an issue of parallel allotment and split of processing resources among concurrent jobs [16].

## 2.3. Contact Network

Contact exists in designated stations. A contact network is a group of persons who can all rapidly get in touch

with one another. It does not have assurance of any type of assistance or access to knowledge. Contact network models endeavor to depict each interactive contact that can possibly lead to disease spread in a community [17]. In this paper, the urban network was used in the contact network analysis, since it offers a high degree of realism.

## 2.4. Urban Contact Network

An urban contact network involves stations like households, shopping centres, religious centres, schools, workplaces, hospitals, and so on in a given community. In the community, every individual which serves as a node or a vertex in the contact network denotes an individual host. An edge or line between two nodes denotes an interaction (that has happened at any point in time for any period) through which disease spread. The number of edges (i.e. contacts) is the node's degree connected to the node [17]. Node degree is a fundamental quantity in network theory. Figure 1 shows individuals contact network in an urban setting.

Figure 1 indicates that all individuals emanate from household. That is individuals from schools, hospitals, workplaces, shopping centres and religious centres originate from households. Quantification of degree of possible contact among individuals in the above places could enhance the knowledge of EVD transmission. The assumptions that were employed to quantify the degree of contact are described in the next paragraph.

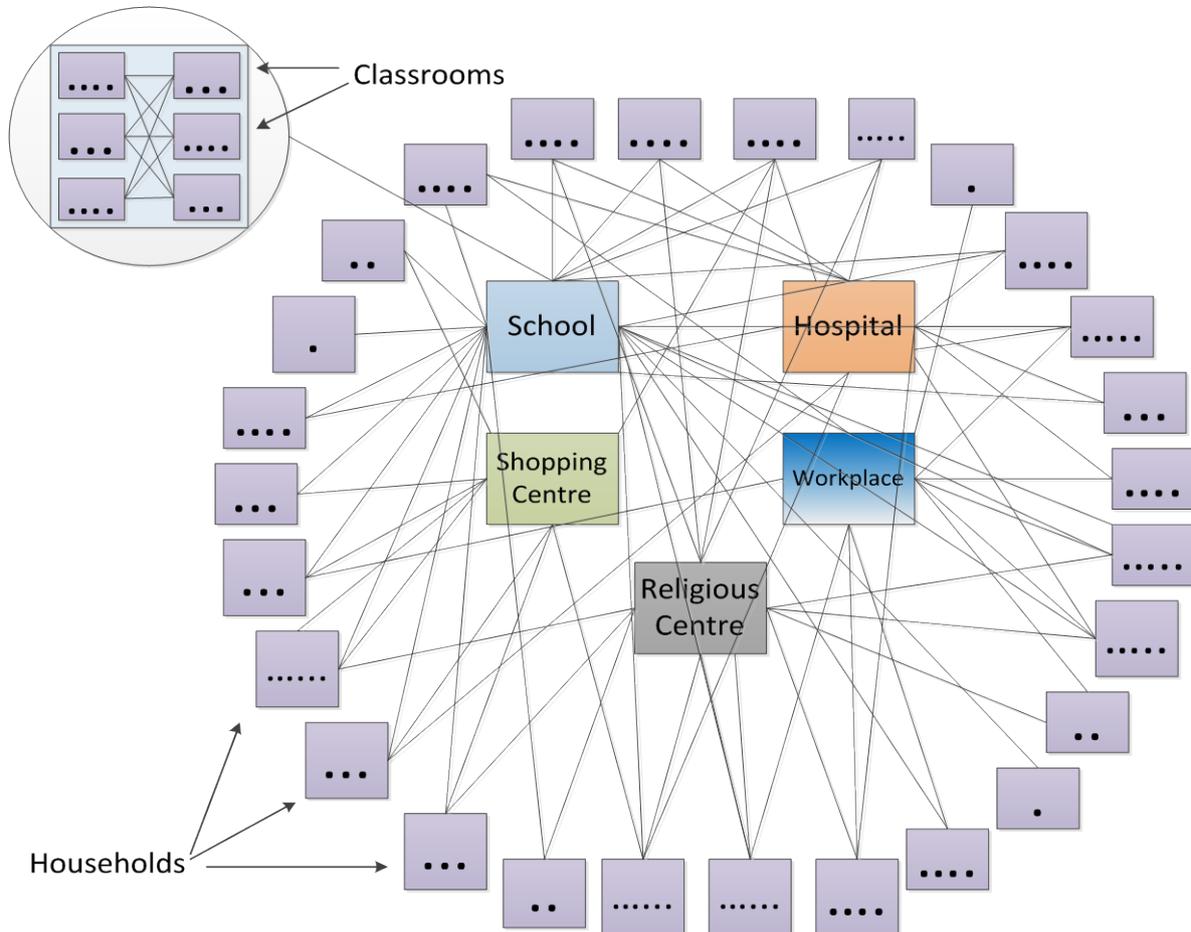


Figure 1. Urban Contact Network

A credible contact network was generated applying computer simulations in this study for an urban location. The data for the country of Liberia was used for simulation. However, households were chosen at random from Liberia household distribution of size  $N=1000$  [2], which generated 5000 persons. The ages of members of households are assigned in accordance with Liberia measured age structure, and then allocated to schools in accordance with school and class distributions size [14]; to occupations in accordance with unemployment data [15], to shopping centres in accordance with business transactions; to hospitals including patients as well as caregivers in accordance with hospital employment as well as bed data [4, 20, 18]; and to religious centres in accordance with data derived from [11]. The above assumptions are also applicable to Guinea and Sierra Leone respectively [8, 9, 22, 23].

Moreover, in each location, a random connection was created between persons with probabilities of 1 for households, 0.35 for schools, 0.25 for hospitals, 0.40 for shopping centres, 0.28 for workplaces and 0.98 for religious centres. Each school or hospital or shopping centre or workplace or religious centre is shared into smaller classrooms or wards or sections or departments or types. Pairs of students or patients or people within these sub-units were related with probability that is higher than

pairs related with sub-units that are not the same. Teachers are allocated to classrooms and related stochastically to suitable students. Caregivers are allocated wards and at this point related to patients appropriately. Shopping centres are allocated to different sections. Workplaces are allocated to different departments and religion is allocated to different types or groups. The probability neighborhood contacts between persons from various households are also low. This network is quite complex but it offers a high degree of realism. Dots denote nodes [5]. That is, persons and lines between dots denote contacts between persons that possibly, could lead to spread of disease. The rate of contact of individuals in the designated stations with respect to population is shown in Figure 2, while the likelihood of transmission of EVD by contact in the designated places is shown in Figure 3. It indicates that the transmission rate decreases in this order: household, religious centre, shopping centre, school, workplace and hospital. The finding supports the idea that all EVD exposed individuals should be gathered in the hospital (Quarantine Centre) since the possibility of spread of the disease is lowest in the hospital. Also, the finding is in line with the submission of Chowell et al [3] that the use of Quarantine Centre for observation and treatment of EVD affected individuals is a dependable control measure of the disease outbreak.

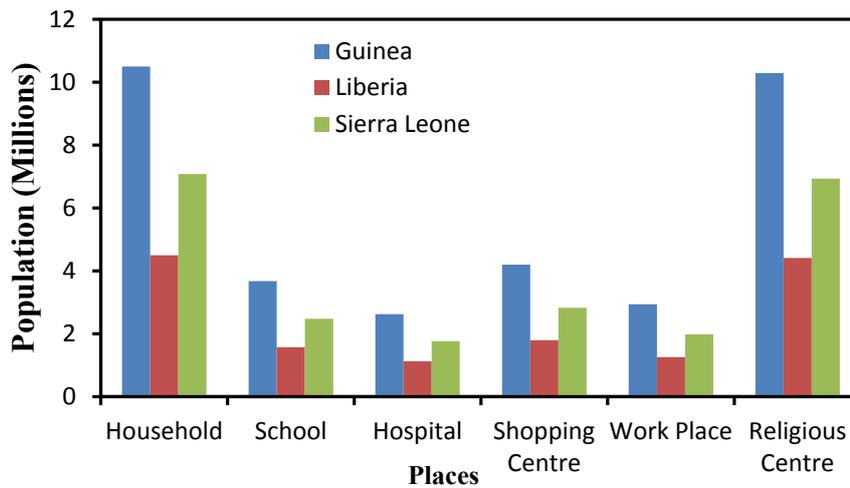


Figure 2. Degree of Contact in the Network Stations

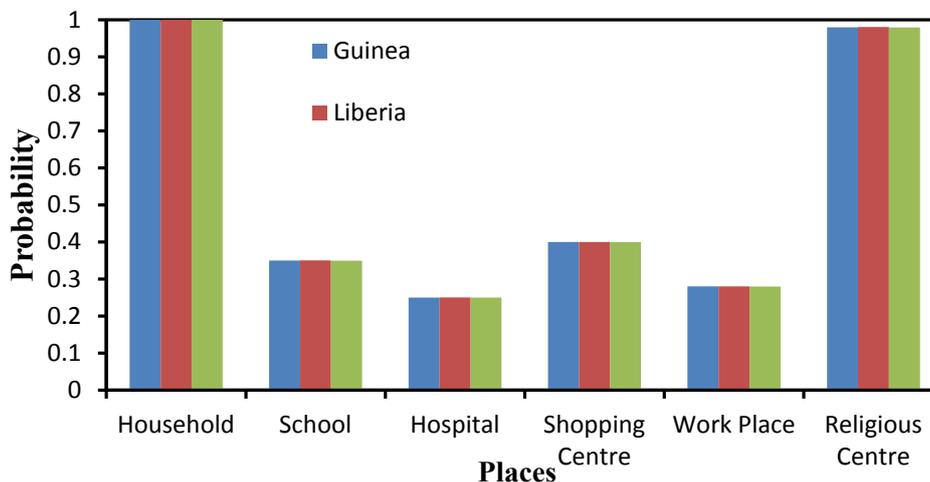


Figure 3. Probability Degree of Contact in the Network Stations

### 3. Transmissibility of EVD.

Transmissibility of a disease  $T$  is the mean probability that an infectious person will transmit the disease to a susceptible person with whom they have contact. Transmissibility  $T$  recaps main facets of transmission of disease as well as the rate at which contacts take place between persons, the probability that a contact will lead to transmission, the duration of the infectious period, and the susceptibility of persons to EVD. Critical transmissibility or epidemic threshold  $T_C$  is the value of transmissibility which a population is vulnerable to large scale epidemics when the basic reproductive number  $R_0$  is 1. According to Meyers et al [17]; Brauer and Castillo-Chavez [10], the basic reproduction number and epidemic threshold is given by

$$R_0 = T \frac{\langle c^2 \rangle}{\langle c \rangle - 1} \tag{1}$$

$$T_C = \frac{\langle c \rangle}{\langle c^2 \rangle - \langle c \rangle} \tag{2}$$

where  $c$  is the mean degree and  $c^2$  is the mean square degree of the network.  $T_C$  is also called the least transmissibility ( $T$ ) necessary for an outbreak to turn into a large scale epidemic.

Cumulative degree distribution against degree of contact for urban contact network is shown in Figure 4. The figure describes the number of contacts (degree) specified on the horizontal axis, which a randomly chosen individual (vertex) possesses.

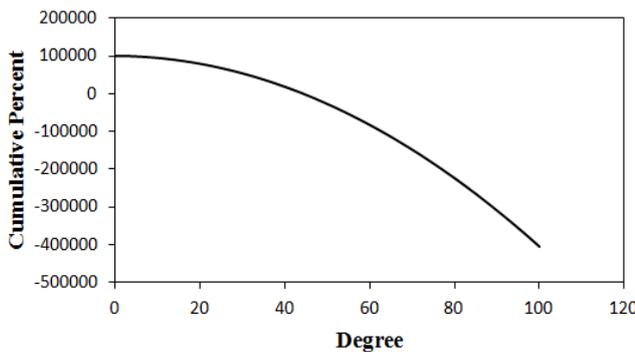


Figure 4. Cumulative Degree Distribution for Urban Contact Network

### 4. Epidemiological Analysis of EVD

Probability Generating Functions (PGF), on the other hand is used to forecast the fate of an outbreak quantity that depicts probability distributions. According to Meyers [17] PGF for a degree distribution is defined as

$$G_0(h) = \sum_{c=1}^{\infty} p_c h^c. \tag{3}$$

The probability of attaining a node or vertex of degree  $c$ , or excess degree  $(c-1)$ , by following a random edge

is proportional to  $c$  and thus, the probability that a vertex at the end of a random edge has excess degree  $(c-1)$  is a constant multiple of  $cp_c$  with the constant chosen to make the sum over  $c$  of the probabilities equal to 1. Then, the probability that a vertex has excess degree  $(c-1)$  is

$$G_1(h) = \frac{\sum_{c=1}^{\infty} cp_c h^{c-1}}{\sum_{c=1}^{\infty} cp_c}. \tag{4}$$

The mean degree equals the derivatives of these terms at  $h=1$  respectively are

$$\langle c \rangle = \sum_{c=1}^{\infty} cp_c \tag{5}$$

and mean excess degree

$$\langle c_e \rangle = \frac{\sum_{c=1}^{\infty} c(c-1)p_c}{\sum_{c=1}^{\infty} cp_c} = \left( \frac{\langle c^2 \rangle}{\langle c \rangle} - 1 \right). \tag{6}$$

Newman [19] derived the value of the epidemic threshold  $T_C$ , the forecasted mean outbreak size  $\langle e \rangle$  and epidemic probability  $E$ . A PGF can be generated for the size of the outbreak through enclosing PGF for new infections number originating from the node or vertex that are infected, and thus, the mean size of an outbreak

$$\langle e \rangle = 1 + \frac{T(c)}{1 - T(c_e)}. \tag{7}$$

Equ. 7 differs once an outbreak turns out to be a large-scale epidemic and it is graded by epidemic threshold  $T_C$ .

The probability of a single infection is considered, which will lead to merely an outbreak (initial value) instead of a full-blown epidemic. Therefore, the full-blown epidemic probability  $E$  is obtained by subtracting the initial value from one

$$E = 1 - \sum_{c=1}^{\infty} p_c (1 + (l-1)T)^c. \tag{8}$$

The individual at the end of an edge or line does not have the disease,  $l$  is the probability at that point and the result is given as

$$l = \frac{\sum_{c=1}^{\infty} cp_c (1 + (l-1)T)^{c-1}}{\sum_{c=1}^{\infty} cp_c}. \tag{9}$$

Full-blown epidemic probability  $E$  and probability of a single infection which will lead to merely an outbreak  $l$ , is solved and these outcomes extended to forecast the outcome of an outbreak based on the number of

individuals that are infected. First person in a community that is infected is known as patient zero. A patient zero with degree  $c$  who will initiate an epidemic at a probability  $r_c$ , is the same as probability that spread of the disease along at least one of the edges originating from the new node or vertex will lead to an epidemic. The probability that the disease does not get transmitted along the edge is  $1-T$ .  $Tl$  is the probability that even if disease is transmitted to the succeeding node or vertex, it does not progress into a full-blown epidemic, for any one of its  $c$  edges. Hence

$$r_c = 1 - (1 - T + Tl)^c \tag{10}$$

The probability that an outbreak of size  $N$  will kindle an epidemic is  $1 - \prod_{i=1}^N (1 - r_{c_i})$ , where  $c_i$  is the degree of person  $i$ . It is done by subtracting one from the probability that none of the  $N$  infected persons flickers an epidemic. The good approximation for the probability of an epidemic is computed likewise, if the number of recent incidents are known but not their contact patterns with each of the  $(1 - r_{c_i})$ 's substituted with the probability that a typical infected person does not flicker an epidemic. The number of edges via which a type of infected person can initiate an epidemic is given by the excess degree PGF, and the probability that any of those edges will not lead to an increase in an epidemic is

$$1 - T + Tl \tag{11}$$

Hence, the probability that no edges will be a channel to an epidemic is

$$\left( \frac{\sum_{c=1}^{\infty} cp_c (1 - T + Tl)^{c-1}}{\sum_{c=1}^{\infty} cp_c} \right), \tag{12}$$

and the probability that an outbreak of size  $N$  flickers an epidemic is

$$1 - \left( \frac{\sum_{c=1}^{\infty} cp_c (1 - T + Tl)^{c-1}}{\sum_{c=1}^{\infty} cp_c} \right)^N \tag{13}$$

Lastly a person's risk of infection for the period of an epidemic as a function of an individual degree was derived. The probability  $f_c$  that a person with degree  $c$  will turn out to be infected for the period of an epidemic is equal to one minus the probability that no individual  $c$  contact will transmit the disease to an individual. The probability that a contact does not transmit the disease is the same to the probability that the contact is infected, but did not transmit the disease,

$$(1-l)(1-T) \tag{14}$$

in addition to the probability that the contact was not infected in the first place,  $l$ . Hence, a randomly selected node or vertex of degree  $c$  will turn out to be infected with probability

$$f_c = r_c = (1 - T + Tl)^c \tag{15}$$

Accordingly, mathematical expressions above are integrated to generate probability of the network (households, religious centres, shopping centres, schools, workplaces and hospitals) infected. Epifire software was used to generate the mean degree  $c$  in urban contact network. The values of transmissibility and their probabilities of network infected for Guinea, Liberia and Sierra Leone are above critical transmissibility (0.0644) and probability of network infected (0.30) before intervention. After intervention, the values reduced which are below critical transmissibility and probability of network infected as shown in Table 1. Figure 5 and Figure 6 show the probability of network infected for dissimilar values of transmissibility before and after intervention respectively. The results indicate that the population was vulnerable to large scale epidemics before intervention in the three countries. The vulnerability decreased drastically after intervention.

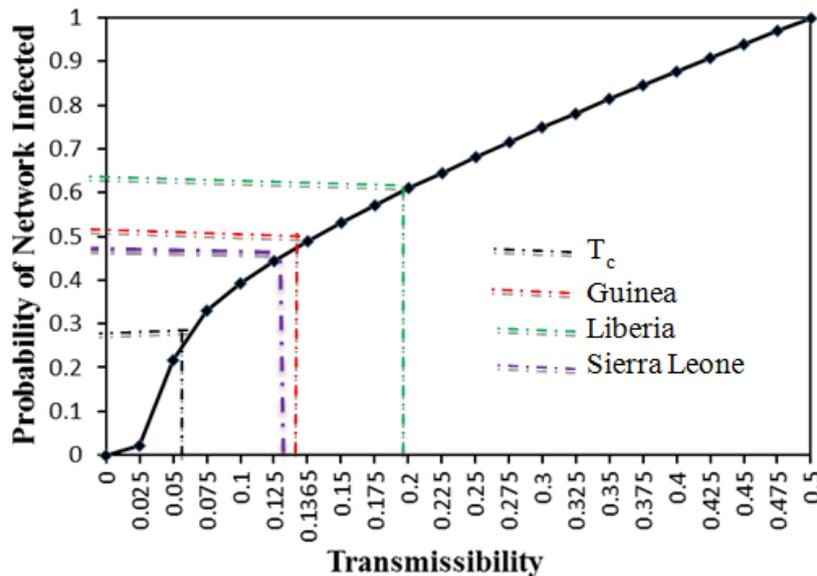


Figure 5. Network simulation for transmissibility before intervention

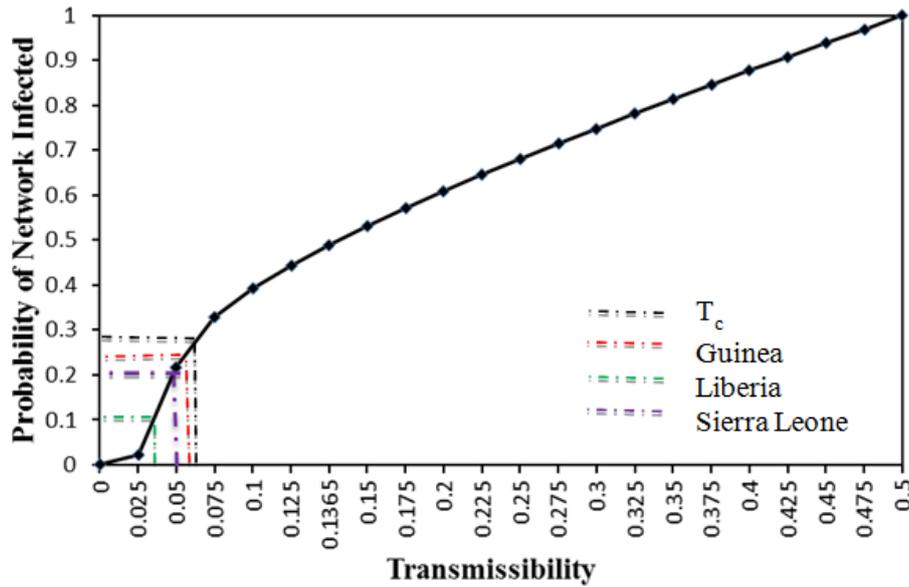


Figure 6. Network simulation for transmissibility after intervention

Table 1. Critical Transmissibility, Transmissibility and Probability of Network of Infected

|  | Country      | Transmissibility | Probability of Network Infected |
|--|--------------|------------------|---------------------------------|
| Before Intervention                                    | Guinea       | 0.1365           | 0.49                            |
|  | Liberia      | 0.2093           | 0.61                            |
|  | Sierra Leone | 0.1325           | 0.47                            |
| After Intervention                                     | Guinea       | 0.0595           | 0.22                            |
|  | Liberia      | 0.0440           | 0.20                            |
|  | Sierra Leone | 0.0571           | 0.21                            |
| Critical Transmissibility = 0.0644, Probability = 0.30 |              |                  |                                 |

### 5. Conclusion

The paper demonstrated the effectiveness of integrating queueing network into SEI<sub>I</sub>ICDR model for EVD. The result for network indicates that the population was vulnerable to large scale epidemics before intervention in the three countries. The  $T_C$  for the three countries was 0.0644. Before intervention, the transmissibility for Guinea was 0.1365, Liberia, 0.2093 and Sierra Leone, 0.1325. After intervention, the transmissibility for Guinea reduced to 0.0595, Liberia, 0.0440 and Sierra Leone, 0.0571. The before and after transmissibility results in comparison with the  $T_C$  indicate that intervention was effective in containing the EVD epidemic. The vulnerability decreased drastically after intervention.

### References

[1] Baskett, F., Chandy, K.M., Muntz, R.R., Palacios, F.G.: Open, Closed and Mixed Networks of Queues with Different Classes of Customers. *J. of the Asso. for Comput. Mach.* 22(2), 249-260 (1975).

[2] Central Intelligence Agency. CIA world factbook. <https://www.cia.gov/library/publications/the-world-factbook/> (2016). Retrieved 2<sup>nd</sup> January 2017.

[3] Chowell, G., Hengartner, N.W., Castillo-Chavez, C., Fenimore, P.W., Hyman, J.M.: The basic reproduction number of Ebola and the effects of public health measures: the cases of Congo and Uganda. *J. of Theoret. Bio.* 229(1), 119-26 (2004).

[4] CHRDR: Centre for Health Research and Diagnostics Guinea. [www.dwu.ac.pg/index.php/centre](http://www.dwu.ac.pg/index.php/centre) (2015). Retrieved 2<sup>nd</sup> January 2017.

[5] De Sterck, H., Miller, T., Manteuffel, T., Sanders, G.: Top-level acceleration of adaptive Algebraic Multilevel Methods for Steady-State Solution to Markov Chains. *Advan. Comput. Math.* 35, 375-403 (2011).

[6] Dike, C.O., Zainuddin, Z.M., Ikeme John Dike, I.J.: Susceptible Infected Removed Epidemic Model Extension for Efficient Analysis of Ebola Virus Disease Transmission. American Scientific Publishers.

[7] Gordon, W.J., Newell, G.F.: Closed queueing systems with exponential servers. *Operations Research.* 15(2), 254-265 (1967).

[8] Guinea Age Structure: [www.indexmundi.com/guinea/age\\_structure.html](http://www.indexmundi.com/guinea/age_structure.html) (2016). Retrieved 2<sup>nd</sup> January 2017.

[9] Guinea Unemployment Rate: <https://www.google.com/webhp?sourceid=chrome-instant&ion=1&espv=2&ie=UTF-8#q=guinea+unemployment+rate> (2017). Retrieved 2<sup>nd</sup> January 2017.

[10] Hernandez-Suarez C.M., Castillo-Chavez C., Lopez O.M., and Hernandez-Cuevas K.: An application of queueing theory to SIS and SEIS epidemic models. *Math. Biosci. and Eng.* 7(4), 809-823 (2010).

[11] International Religious Freedom Report: Liberia. United States Department of State, November 17, 2010. <http://www.state.gov/g/drl/rls/irf/2010/148698.htm>. Retrieved October 9, 2016.

[12] Jackson, J.R.: Jobshop-like queueing systems, management science. 10(1), 131-142 (1963).

[13] Kelly, F. P.: Networks of queues with customers of different types. *J. of Appl. Probab.* 12, 542-554 (1975).

[14] Liberia Age Structure: [www.indexmundi.com/liberia/age\\_structure.html](http://www.indexmundi.com/liberia/age_structure.html) (2016). Retrieved 2<sup>nd</sup> January 2017.

- [15] Liberia Unemployment Rate: <https://www.google.com/webhp?sourceid=chrome-instant&ion=1&espv=2&ie=UTF-8#q=liberia+unemployment+rate> (2017). Retrieved 2<sup>nd</sup> January 2017.
- [16] Liu, Y.: Queueing networks as models of human performance and human-computer interaction. Proceedings of the 1994 Symposium on Human Interaction with Complex Systems. Department of Industrial and Operations Engineering, University of Michigan, USA. Technical Report 93-32. 1-15.
- [17] Meyers, L.A., Pourbohloul, B., Newman, M.E.J., Skowronski, D.M., Brunham, R.C.: Network theory and SARS: Predicting outbreak diversity. *J. of Theoret. Bio.* 232(1), 71-81 (2005).
- [18] MIDC: Establishment of Medical Imaging and Diagnostic Centre in Freetown. [www.rvo.nl>projecten>establishment](http://www.rvo.nl/projecten/establishment) (2009). Retrieved 2<sup>nd</sup> January 2017.
- [19] Newman, M.E.J. (2002). The spread of epidemic disease on networks. *Phys. Review E.* 66, 016128.
- [20] NPHIL: National Public Health Institute of Liberia. [www.ianphi.org>newprofiles>liberia](http://www.ianphi.org/newprofiles/liberia) (2014). Retrieved 2<sup>nd</sup> January 2017.
- [21] Ross, S.M. Introduction to probability models. (9<sup>th</sup> ed.). Academic Press, Elsevier Inc.: USA (2007)
- [22] Sierra Leone Age Structure: [www.indexmundi.com/sierra\\_leone/age\\_structure.html](http://www.indexmundi.com/sierra_leone/age_structure.html) (2016). Retrieved 2<sup>nd</sup> January 2017.
- [23] Sierra Leone Unemployment Rate: <https://www.google.com/webhp?sourceid=chrome-instant&ion=1&espv=2&ie=UTF-8#q=sierra+leone+unemployment+rate> (2017). Retrieved 2<sup>nd</sup> January 2017.
- [24] Sztrik, J.: Basic Queueing Theory. <http://irh.inf.unideb.hu/user/jsztrik> (2012). Retrieved September, 2015.